GCGGACGCGT GGGTGAAATT GAAAATCAAG ATAAAAATGT TCACAATTAA 50
GCTCCTTCTT TTTATTGTTC CTCTAGTTAT TTCCTCCAGA ATTGATCAAG 100
ACAATTCATC ATTTGATTCT CTATCTCCAG AGCCAAAATC AAGATTTGCT 150
ATGTTAGACG ATGTAAAAAT TTTAGCCAAT GGCCTCCTTC AGTTGGGACA 200
TGGTCTTAAA GACTTTGTCC ATAAGACGAA GGGCCAAATT AATGACATAT 250
TTCAAAAACT CAACATATTT GATCAGTCTT TTTATGATCT ATCGCTGCAA 300
ACCAGTGAAA TCAAAGAAGA AGAAAAGGAA CTGAGAAGAA CTACATATAA 350
ACTACAAGTC AAAAATGAAG AGGTAAAGAA TATGTCACTT GAACTCAACT 400
CAAAACTTGA AAGCCTCCTA GAAGAAAAAA TTCTACTTCA ACAAAAAGTG 450
AAATATTTAG AAGAGCAACT AACTAACTTA ATTCAAAATC AACCTGAAAC 500
TCCAGAACAC CCAGAAGTAA CTTCACTTAA AACTTTTGTA GAAAAACAAG 550
ATAATAGCAT CAAAGACCTT CTCCAGACCG TGGAAGACCA ATATAAACAA 600
TTAAACCAAC AGCATAGTCA AATAAAAGAA ATAGAAAATC AGCTCAGAAG 650
GACTAGTATT CAAGAACCCA CAGAAATTTC TCTATCTTCC AAGCCAAGAG 700
CACCAAGAAC TACTCCCTTT CTTCAGTTGA ATGAAATAAG AAATGTAAAA 750
CATGATGGCA TTCCTGCTGA ATGTACCACC ATTTATAACA GAGGTGAACA 800
TACAAGTGGC ATGTATGCCA TCAGACCCAG CAACTCTCAA GTTTTTCATG 850
TCTACTGTGA TGTTATATCA GGTAGTCCAT GGACATTAAT TCAACATCGA 900
ATAGATGGAT CACAAAACTT CAATGAAACG TGGGAGAACT ACAAATATGG 950
TTTTGGGAGG CTTGATGGAG AATTTTGGTT GGGCCTAGAG AAGATATACT 1000
CCATAGTGAA GCAATCTAAT TATGTTTTAC GAATTGAGTT GGAAGACTGG 1050
AAAGACAACA AACATTATAT TGAATATTCT TTTTACTTGG GAAATCACGA 1100
AACCAACTAT ACGCTACATC TAGTTGCGAT TACTGGCAAT GTCCCCAATG 1150
CAATCCCGGA AAACAAAGAT TTGGTGTTTT CTACTTGGGA TCACAAAGCA 1200
AAAGGACACT TCAACTGTCC AGAGGGTTAT TCAGGAGGCT GGTGGTGGCA 1250

FIG. 1A-1

TGATGAGTGT GGAGAAAACA ACCTAAATGG TAAATATAAC AAACCAAGAG 1300

CAAAATCTAA GCCAGAGAGG AGAAGAGGAT TATCTTGGAA GTCTCAAAAT 1350

GGAAGGTTAT ACTCTATAAA ATCAACCAAA ATGTTGATCC ATCCAACAGA 1400

TTCAGAAAGC TTTGAATGAA CTGAGGCAAT TTAAAGGCAT ATTTAACCAT 1450

TAACTCATTC CAAGTTAATG TGGTCTAATA ATCTGGTATA AATCCTTAAG 1500

AGAAAGCTTG AGAAATAGAT TTTTTTTATC TTAAAGTCAC TGTCTATTTA 1550

AGATTAAACA TACAATCACA TAACCTTAAA GAATACCGTT TACATTTCTC 1600

AATCAAAATT CTTATAATAC TATTTGTTTT AAATTTTGTG ATGTGGGAAT 1650

CAATTTTAGA TGGTCACAAT CTAGATTATA ATCAATAGGT GAACTTATTA 1700

AATAACTTTT CTAAATAAAA AATTTAGAGA CTTTTATTTT AAAAGGCATC 1750

ATATGAGCTA ATATCACAAC TTTCCCAGTT TAAAAAACTA GTACTCTTGT 1800

TAAAACTCTA AACTTGACTA AATACAGAGG ACTGGTAATT GTACAGTTCT 1850

TAAATGTTGT AGTATTAATT TCAAAACTAA AAATCGTCAG CACAGAGTAT 1900

GTGTAAAAAT CTGTAATACA AATTTTTAAA CTGATGCTTC ATTTTGCTAC 1950

AAAATAATTT GGAGTAAATG TTTGATATGA TTTATTTATG AAACCTAATG 2000

AAGCAGAATT AAATACTGTA TTAAAATAAG TTCGCTGTCT TT 2042

FIG. 1A-2

Met	Phe	Thr	Ile	Lys	Leu	Leu	Leu	Phe	Ile	Val	Pro	Leu	Val	Ile
1				5					10					15
Ser	Ser	Arg	Ile	Asp	Gln	Asp	Asn	Ser	Ser	Phe	Asp	Ser	Leu	Ser
				20					25					30
Pro	Glu	Pro	Lys	Ser	Arg	Phe	Ala	Met	Leu	Asp	Asp	Val	Lys	Ile
				35					40					45
Leu	Ala	Asn	Gly	Leu	Leu	Gln	Leu	Gly	His	Gly	Leu	Lys	Asp	Phe
				50					55					60
Val	His	Lys	Thr	Lys	Gly	Gln	Ile	Asn	Asp	Ile	Phe	Gln	Lys	Leu
				65					70					75
Asn	Ile	Phe	Asp	Gln	Ser	Phe	Tyr	Asp	Leu	Ser	Leu	Gln	Thr	Ser
				80					85					90
Glu	Ile	Lys	Glu	Glu	Glu	Lys	Glu	Leu	Arg	Arg	Thr	Thr	Tyr	Lys
				95					100					105
Leu	Gln	Val	Lys	Asn	Glu	Glu	Val	Lys	Asn	Met	Ser	Leu	Glu	Leu
				110					115					120
Asn	Ser	Lys	Leu	Glu	Ser	Leu	Leu	Glu	Glu	Lys	Ile	Leu	Leu	Gln
				125					130					135
Gln	Lys	Val	Lys	Tyr	Leu	Glu	Glu	Gln	Leu	Thr	Asn	Leu	Ile	Gln
				140					145					150
Asn	Gln	Pro	Glu	Thr	Pro	Glu	His	Pro	Glu	Val	Thr	Ser	Leu	Lys
				155					160					165
Thr	Phe	Val	Glu	Lys	Gln	Asp	Asn	Ser	Ile	Lys	Asp	Leu	Leu	Gln
				170					175					180
Thr	Val	Glu	Asp	Gln	Tyr	Lys	Gln	Leu	Asn	Gln	Gln	His	Ser	Gln
				185					190					195
Ile	Lys	Glu	Ile	Glu	Asn	Gln	Leu	Arg	Arg	Thr	Ser	Ile	Gln	Glu
				200					205					210
Pro	Thr	Glu	Ile	Ser	Leu	Ser	Ser	Lys	Pro	Arg	Ala	Pro	Arg	Thr
				215					220					225
Thr	Pro	Phe	Leu	Gln	Leu	Asn	Glu	Ile	Arg	Asn	Val	Lys	His	Asp
				230					235					240

FIG. 1B-1

Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His
245 250 255

Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe
260 265 270

His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile
275 280 285

Gln His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu
290 295 300

Asn Tyr Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu
305 310 315

Gly Leu Glu Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val
320 325 330

Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile
335 340 345

Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr Asn Tyr Thr Leu
350 355 360

His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala Ile Pro Glu
365 370 375

Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala Lys Gly
380 385 390

His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp His
395 400 405

Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro
410 415 420

Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu Ser Trp Lys
425 430 435

Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu
440 445 450

Ile His Pro Thr Asp Ser Glu Ser Phe Glu
455 460

FIG. 1B-2

GGCTGAGGGG AGGCCCGGAG CCTTTCTGGG GCCTGGGGGA TCCTCTTGCA 50

CTGGTGGGTG GAGAGAAGCG CCTGCAGCCA ACCAGGGTCA GGCTGTGCTC 100

ACAGTTTCCT CTGGCGGCAT GTAAAGGCTC CACAAAGGAG TTGGGAGTTC 150

AAATGAGGCT GCTGCGGACG GCCTGAGGAT GGACCCCAAG CCCTGGACCT 200

GCCGAGCGTG GCACTGAGGC AGCGGCTGAC GCTACTGTGA GGGAAAGAAG 250

GTTGTGAGCA GCCCCGCAGG ACCCCTGGCC AGCCCTGGCC CCAGCCTCTG 300

CCGGAGCCCT CTGTGGAGGC AGAGCCAGTG GAGCCCAGTG AGGCAGGGCT 350

GCTTGGCAGC CACCGGCCTG CAACTCAGGA ACCCCTCCAG AGGCCATGGA 400

CAGGCTGCCC CGCTGACGGC CAGGGTGAAG CATGTGAGGA GCCGCCCCGG 450

AGCCAAGCAG GAGGGAAGAG GCTTTCATAG ATTCTATTCA CAAAGAATAA 500

CCACCATTTT GCAAGGACCA TGAGGCCACT GTGCGTGACA TGCTGGTGGC 550

TCGGACTGCT GGCTGCCATG GGAGCTGTTG CAGGCCAGGA GGACGGTTTT 600

GAGGGCACTG AGGAGGGCTC GCCAAGAGAG TTCATTTACC TAAACAGGTA 650

CAAGCGGGCG GGCGAGTCCC AGGACAAGTG CACCTACACC TTCATTGTGC 700

CCCAGCAGCG GGTCACGGGT GCCATCTGCG TCAACTCCAA GGAGCCTGAG 750

GTGCTTCTGG AGAACCGAGT GCATAAGCAG GAGCTAGAGC TGCTCAACAA 800

TGAGCTGCTC AAGCAGAAGC GGCAGATCGA GACGCTGCAG CAGCTGGTGG 850

AGGTGGACGG CGGCATTGTG AGCGAGGTGA AGCTGCTGCG CAAGGAGAGC 900

CGCAACATGA ACTCGCGGGT CACGCAGCTC TACATGCAGC TCCTGCACGA 950

GATCATCCGC AAGCGGGACA ACGCGTTGGA GCTCTCCCAG CTGGAGAACA 1000

GGATCCTGAA CCAGACAGCC GACATGCTGC AGCTGGCCAG CAAGTACAAG 1050

GACCTGGAGC ACAAGTACCA GCACCTGGCC ACACTGGCCC ACAACCAATC 1100

AGAGATCATC GCGCAGCTTG AGGAGCACTG CCAGAGGGTG CCCTCGGCCA 1150

GGCCCGTCCC CCAGCCACCC CCCGCTGCCC CGCCCCGGGT CTACCAACCA 1200

FIG. 2A

CCCACCTACA ACCGCATCAT CAACCAGATC TCTACCAACG AGATCCAGAG 1250

TGACCAGAAC CTGAAGGTGC TGCCACCCCC TCTGCCCACT ATGCCCACTC 1300

TCACCAGCCT CCCATCTTCC ACCGACAAGC CGTCGGGCCC ATGGAGAGAC 1350

TGCCTGCAGG CCCTGGAGGA TGGCCACGAC ACCAGCTCCA TCTACCTGGT 1400

GAAGCCGGAG AACACCAACC GCCTCATGCA GGTGTGGTGC GACCAGAGAC 1450

ACGACCCCGG GGGCTGGACC GTCATCCAGA GACGCCTGGA TGGCTCTGTT 1500

AACTTCTTCA GGAACTGGGA GACGTACAAG CAAGGGTTTG GGAACATTGA 1550

CGGCGAATAC TGGCTGGGCC TGGAGAACAT TTACTGGCTG ACGAACCAAG 1600

GCAACTACAA ACTCCTGGTG ACCATGGAGG ACTGGTCCGG CCGCAAAGTC 1650

TTTGCAGAAT ACGCCAGTTT CCGCCTGGAA CCTGAGAGCG AGTATTATAA 1700

GCTGCGGCTG GGGCGCTACC ATGGCAATGC GGGTGACTCC TTTACATGGC 1750

ACAACGGCAA GCAGTTCACC ACCCTGGACA GAGATCATGA TGTCTACACA 1800

GGAAACTGTG CCCACTACCA GAAGGGAGGC TGGTGGTATA ACGCCTGTGC 1850

CCACTCCAAC CTCAACGGGG TCTGGTACCG CGGGGGCCAT TACCGGAGCC 1900

GCTACCAGGA CGGAGTCTAC TGGGCTGAGT TCCGAGGAGG CTCTTACTCA 1950

CTCAAGAAAG TGGTGATGAT GATCCGACCG AACCCCAACA CCTTCCACTA 2000

AGCCAGCTCC CCCTCCTGAC CTCTCGTGGC CATTGCCAGG AGCCCACCCT 2050

GGTCACGCTG GCCACAGCAC AAAGAACAAC TCCTCACCAG TTCATCCTGA 2100

GGCTGGGAGG ACCGGGATGC TGGATTCTGT TTTCCGAAGT CACTGCAGCG 2150

GATGATGGAA CTGAATCGAT ACGGTGTTTT CTGTCCCTCC TACTTTCCTT 2200

CACACCAGAC AGCCCCTCAT GTCTCCAGGA CAGGACAGGA CTACAGACAA 2250

CTCTTTCTTT AAATAAATTA AGTCTCTACA ATAAAAAAAA 2290

FIG. 2B

Met	Arg	Pro	Leu	Cys	Val	Thr	Cys	Trp	Trp	Leu	Gly	Leu	Leu	Ala
1				5					10					15
Ala	Met	Gly	Ala	Val	Ala	Gly	Gln	Glu	Asp	Gly	Phe	Glu	Gly	Thr
				20					25					30
Glu	Glu	Gly	Ser	Pro	Arg	Glu	Phe	Ile	Tyr	Leu	Asn	Arg	Tyr	Lys
				35					40					45
Arg	Ala	Gly	Glu	Ser	Gln	Asp	Lys	Cys	Thr	Tyr	Thr	Phe	Ile	Val
				50					55					60
Pro	Gln	Gln	Arg	Val	Thr	Gly	Ala	Ile	Cys	Val	Asn	Ser	Lys	Glu
				65					70					75
Pro	Glu	Val	Leu	Leu	Glu	Asn	Arg	Val	His	Lys	Gln	Glu	Leu	Glu
				80					85					90
Leu	Leu	Asn	Asn	Glu	Leu	Leu	Lys	Gln	Lys	Arg	Gln	Ile	Glu	Thr
				95					100					105
Leu	Gln	Gln	Leu	Val	Glu	Val	Asp	Gly	Gly	Ile	Val	Ser	Glu	Val
				110					115					120
Lys	Leu	Leu	Arg	Lys	Glu	Ser	Arg	Asn	Met	Asn	Ser	Arg	Val	Thr
				125					130					135
Gln	Leu	Tyr	Met	Gln	Leu	Leu	His	Glu	Ile	Ile	Arg	Lys	Arg	Asp
				140					145					150
Asn	Ala	Leu	Glu	Leu	Ser	Gln	Leu	Glu	Asn	Arg	Ile	Leu	Asn	Gln
				155					160					165
Thr	Ala	Asp	Met	Leu	Gln	Leu	Ala	Ser	Lys	Tyr	Lys	Asp	Leu	Glu
				170					175					180
His	Lys	Tyr	Gln	His	Leu	Ala	Thr	Leu	Ala	His	Asn	Gln	Ser	Glu
				185					190					195
Ile	Ile	Ala	Gln	Leu	Glu	Glu	His	Cys	Gln	Arg	Val	Pro	Ser	Ala
				200					205					210
Arg	Pro	Val	Pro	Gln	Pro	Pro	Pro	Ala	Ala	Pro	Pro	Arg	Val	Tyr
				215					220					225
Gln	Pro	Pro	Thr	Tyr	Asn	Arg	Ile	Ile	Asn	Gln	Ile	Ser	Thr	Asn
				230					235					240
Glu	Ile	Gln	Ser	Asp	Gln	Asn	Leu	Lys	Val	Leu	Pro	Pro	Pro	Leu
				245					250					255

FIG. 3A

Pro Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys
260 265 270

Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly
275 280 285

His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn
290 295 300

Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly
305 310 315

Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe
320 325 330

Arg Asn Trp Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly
335 340 345

Glu Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln
350 355 360

Gly Asn Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg
365 370 375

Lys Val Phe Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser
380 385 390

Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly
395 400 405

Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe Thr Thr Leu Asp
410 415 420

Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His Tyr Gln Lys
425 430 435

Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu Asn Gly
440 445 450

Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp Gly
455 460 465

Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys
470 475 480

Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
485 490 493

FIG. 3B

GCAGCTGGTT ACTGCATTTC TCCATGTGGC AGACAGAGCA AAGCCACAAC 50

GCTTTCTCTG CTGGATTAAA GACGGCCCAC AGACCAGAAC TTCCACTATA 100

CTACTTAAAA TTACATAGGT GGCTTGTCAA ATTCAATTGA TTAGTATTGT 150

AAAAGGAAAA AGAAGTTCCT TCTTACAGCT TGGATTCAAC GGTCCAAAAC 200

AAAAATGCAG CTGCCATTAA AGTCTCAGAT GAACAAACTT CTACACTGAT 250

TTTTAAAATC AAGAATAAGG GCAGCAAGTT TCTGGATTCA CTGAATCAAC 300

AGACACAAAA AGCTGGCAAT ATAGCAACTA TGAAGAGAAA AGCTACTAAT 350

AAAATTAACC CAACGCATAG AAGACTTTTT TTTCTCTTCT AAAAACAACT 400

AAGTAAAGAC TTAAATTTAA ACACATCATT TTACAACCTC ATTTCAAAAT 450

GAAGACTTTT ACCTGGACCC TAGGTGTGCT ATTCTTCCTA CTAGTGGACA 500

CTGGACATTG CAGAGGTGGA CAATTCAAAA TTAAAAAAAT AAACCAGAGA 550

AGATACCCTC GTGCCACAGA TGGTAAAGAG GAAGCAAAGA AATGTGCATA 600

CACATTCCTG GTACCTGAAC AAAGAATAAC AGGGCCAATC TGTGTCAACA 650

CCAAGGGGCA AGATGCAAGT ACCATTAAAG ACATGATCAC CAGGATGGAC 700

CTTGAAAACC TGAAGGATGT GCTCTCCAGG CAGAAGCGGG AGATAGATGT 750

TCTGCAACTG GTGGTGGATG TAGATGGAAA CATTGTGAAT GAGGTAAAGC 800

TGCTGAGAAA GGAAAGCCGT AACATGAACT CTCGTGTTAC TCAACTCTAT 850

ATGCAATTAT TACATGAGAT TATCCGTAAG AGGGATAATT CACTTGAACT 900

TTCCCAACTG GAAAACAAAA TCCTCAATGT CACCACAGAA ATGTTGAAGA 950

TGGCAACAAG ATACAGGGAA CTAGAGGTGA AATACGCTTC CTTGACTGAT 1000

CTTGTCAATA ACCAATCTGT GATGATCACT TTGTTGGAAG AACAGTGCTT 1050

GAGGATATTT TCCCGACAAG ACACCCATGT GTCTCCCCCA CTTGTCCAGG 1100

TGGTGCCACA ACATATTCCT AACAGCCAAC AGTATACTCC TGGTCTGCTG 1150

GGAGGTAACG AGATTCAGAG GGATCCAGGT TATCCCAGAG ATTTAATGCC 1200

FIG. 4A

ACCACCTGAT CTGGCAACTT CTCCCACCAA AAGCCCTTTC AAGATACCAC 1250

CGGTAACTTT CATCAATGAA GGACCATTCA AAGACTGTCA GCAAGCAAAA 1300

GAAGCTGGGC ATTCGGTCAG TGGGATTTAT ATGATTAAAC CTGAAAACAG 1350

CAATGGACCA ATGCAGTTAT GGTGTGAAAA CAGTTTGGAC CCTGGGGGTT 1400

GGACTGTTAT TCAGAAAAGA ACAGACGGCT CTGTCAACTT CTTCAGAAAT 1450

TGGGAAAATT ATAAGAAAGG GTTTGGAAAC ATTGACGGAG AATACTGGCT 1500

TGGACTGGAA AATATCTATA TGCTTAGCAA TCAAGATAAT TACAAGTTAT 1550

TGATTGAATT AGAAGACTGG AGTGATAAAA AAGTCTATGC AGAATACAGC 1600

AGCTTTCGTC TGGAACCTGA AAGTGAATTC TATAGACTGC GCCTGGGAAC 1650

TTACCAGGGA AATGCAGGGG ATTCTATGAT GTGGCATAAT GGTAAACAAT 1700

TCACCACACT GGACAGAGAT AAAGATATGT ATGCAGGAAA CTGCGCCCAC 1750

TTTCATAAAG GAGGCTGGTG GTACAATGCC TGTGCACATT CTAACCTAAA 1800

TGGAGTATGG TACAGAGGAG GCCATTACAG AAGCAAGCAC CAAGATGGAA 1850

TTTTCTGGGC CGAATACAGA GGCGGGTCAT ACTCCTTAAG AGCAGTTCAG 1900

ATGATGATCA AGCCTATTGA CTGAAGAGAG ACACTCGCCA ATTTAAATGA 1950

CACAGAACTT TGTACTTTTC AGCTCTTAAA AATGTAAATG TTACATGTAT 2000

ATTACTTGGC ACAATTTATT TCTACACAGA AAGTTTTTAA AATGAATTTT 2050

ACCGTAACTA TAAAAGGGAA CCTATAAATG TAGTTTCATC TGTCGTCAAT 2100

TACTGCAGAA AATTATGTGT ATCCACAACC TAGTTATTTT AAAAATTATG 2150

TTGACTAAAT ACAAAGTTTG TTTTCTAAAA TGTAAATATT TGCCACAATG 2200

TAAAGCAAAT CTTAGCTATA TTTTAAATCA TAAATAACAT GTTCAAGATA 2250

CTTAACAATT TATTTAAAAT CTAAGATTGC TCTAACGTCT AGTGAAAAAA 2300

ATATTTTTTA AATTTCAGCC AAATAATGCA TTTTATTTTA TAAAAATACA 2350

GACAGAAAAT TAGGGAGAAA CTTCTAGTTT TGCCAATAGA AAATGTTCTT 2400

FIG. 4B

CCATTGAATA AAAGTTATTT CAAATTGAAT TTGTGCCTTT CACACGTAAT 2450

GATTAAATCT GAATTCTTAA TAATATATCC TATGCTGATT TTCCCAAAAC 2500

ATGACCCATA GTATTAAATA CATATCATTT TTAAAAATAA AAAAAAACCC 2550

AAAAATAATG CATGCATAAT TTAAATGGTC AATTTATAAA GACAAATCTA 2600

TGAATGAATT TTTCAGTGTT ATCTTCATAT GATATGCTGA ACACCAAAAT 2650

CTCCAGAAAT GCATTTTATG TAGTTCTAAA ATCAGCAAAA TATTGGTATT 2700

ACAAAAATGC AGAATATTTA GTGTGCTACA GATCTGAATT ATAGTTCTAA 2750

TTTATTATTA CTTTTTTTCT AATTTACTGA TCTTACTACT ACAAAGAAAA 2800

AAAAACCCAA CCCATCTGCA ATTCAAATCA GAAAGTTTGG ACAGCTTTAC 2850

AAGTATTAGT GCATGCTCAG AACAGGTGGG ACTAAAACAA ACTCAAGGAA 2900

CTGTTGGCTG TTTTCCCGAT ACTGAGAATT CAACAGCTCC AGAGCAGAAG 2950

CCACAGGGGC ATAGCTTAGT CCAAACTGCT AATTTCATTT TACAGTGTAT 3000

GTAACGCTTA GTCTCACAGT GTCTTTAACT CATCTTTGCA ATCAACAACT 3050

TTACTAGTGA CTTTCTGGAA CAATTTCCTT TCAGGAATAC ATATTCACTG 3100

CTTAGAGGTG ACCTTGCCTT AATATATTTG TGAAGTTAAA ATTTTAAAGA 3150

TAGCTCATGA AACTTTTGCT TAAGCAAAAA GAAAACCTCG AATTGAAATG 3200

TGTGAGGCAA ACTATGCATG GGAATAGCTT AATGTGAAGA TAATCATTTG 3250

GACAACTCAA ATCCATCAAC ATGACCAATG TTTTTCATCT GCCACATCTC 3300

AAAATAAAAC TTCTGGTGAA ACAAATTAAA CAAAATATCC AAACCTCAAA 3350

AAAAA 3355

FIG. 4C

Met	Lys	Thr	Phe	Thr	Trp	Thr	Leu	Gly	Val	Leu	Phe	Phe	Leu	Leu
1				5					10					15
Val	Asp	Thr	Gly	His	Cys	Arg	Gly	Gly	Gln	Phe	Lys	Ile	Lys	Lys
				20					25					30
Ile	Asn	Gln	Arg	Arg	Tyr	Pro	Arg	Ala	Thr	Asp	Gly	Lys	Glu	Glu
				35					40					45
Ala	Lys	Lys	Cys	Ala	Tyr	Thr	Phe	Leu	Val	Pro	Glu	Gln	Arg	Ile
				50					55					60
Thr	Gly	Pro	Ile	Cys	Val	Asn	Thr	Lys	Gly	Gln	Asp	Ala	Ser	Thr
				65					70					75
Ile	Lys	Asp	Met	Ile	Thr	Arg	Met	Asp	Leu	Glu	Asn	Leu	Lys	Asp
				80					85					90
Val	Leu	Ser	Arg	Gln	Lys	Arg	Glu	Ile	Asp	Val	Leu	Gln	Leu	Val
				95					100					105
Val	Asp	Val	Asp	Gly	Asn	Ile	Val	Asn	Glu	Val	Lys	Leu	Leu	Arg
				110					115					120
Lys	Glu	Ser	Arg	Asn	Met	Asn	Ser	Arg	Val	Thr	Gln	Leu	Tyr	Met
				125					130					135
Gln	Leu	Leu	His	Glu	Ile	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Leu	Glu
				140					145					150
Leu	Ser	Gln	Leu	Glu	Asn	Lys	Ile	Leu	Asn	Val	Thr	Thr	Glu	Met
				155					160					165
Leu	Lys	Met	Ala	Thr	Arg	Tyr	Arg	Glu	Leu	Glu	Val	Lys	Tyr	Ala
				170					175					180
Ser	Leu	Thr	Asp	Leu	Val	Asn	Asn	Gln	Ser	Val	Met	Ile	Thr	Leu
				185					190					195
Leu	Glu	Glu	Gln	Cys	Leu	Arg	Ile	Phe	Ser	Arg	Gln	Asp	Thr	His
				200					205					210
Val	Ser	Pro	Pro	Leu	Val	Gln	Val	Val	Pro	Gln	His	Ile	Pro	Asn
				215					220					225
Ser	Gln	Gln	Tyr	Thr	Pro	Gly	Leu	Leu	Gly	Gly	Asn	Glu	Ile	Gln
				230					235					240
Arg	Asp	Pro	Gly	Tyr	Pro	Arg	Asp	Leu	Met	Pro	Pro	Pro	Asp	Leu
				245					250					255

FIG. 5A

Ala Thr Ser Pro Thr Lys Ser Pro Phe Lys Ile Pro Pro Val Thr
260 265 270

Phe Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys Glu
275 280 285

Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn
290 295 300

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro
305 310 315

Gly Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn
320 325 330

Phe Phe Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile
335 340 345

Asp Gly Glu Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser
350 355 360

Asn Gln Asp Asn Tyr Lys Leu Leu Ile Glu Leu Glu Asp Trp Ser
365 370 375

Asp Lys Lys Val Tyr Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro
380 385 390

Glu Ser Glu Phe Tyr Arg Leu Arg Leu Gly Thr Tyr Gln Gly Asn
395 400 405

Ala Gly Asp Ser Met Met Trp His Asn Gly Lys Gln Phe Thr Thr
410 415 420

Leu Asp Arg Asp Lys Asp Met Tyr Ala Gly Asn Cys Ala His Phe
425 430 435

His Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu
440 445 450

Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys His Gln
455 460 465

Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly Ser Tyr Ser Leu
470 475 480

Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp
485 490 491

FIG. 5B

GGCTCAGAGG CCCCACTGGA CCCTCGGCTC TTCCTTGGAC TTCTTGTGTG 50

TTCTGTGAGC TTCGCTGGAT TCAGGGTCTT GGGCATCAGA GGTGAGAGGG 100

TGGGAAGGTC CGCCGCGATG GGGAAGCCCT GGCTGCGTGC GCTACAGCTG 150

CTGCTCCTGC TGGGCGCGTC GTGGGCGCGG GCGGGCGCCC CGCGCTGCAC 200

CTACACCTTC GTGCTGCCCC CGCAGAAGTT CACGGGCGCT GTGTGCTGGA 250

GCGGCCCCGC ATCCACGCGG GCGACGCCCG AGGCCGCCAA CGCCAGCGAG 300

CTGGCGGCGC TGCGCATGCG CGTCGGCCGC CACGAGGAGC TGTTACGCGA 350

GCTGCAGAGG CTGGCGGCGG CCGACGGCGC CGTGGCCGGC GAGGTGCGCG 400

CGCTGCGCAA GGAGAGCCGC GGCCTGAGCG CGCGCCTGGG CCAGTTGCGC 450

GCGCAGCTGC AGCACGAGGC GGGGCCCGGG GCGGGCCCGG GGGCGGATCT 500

GGGGGCGGAG CCTGCCGCGG CGCTGGCGCT GCTCGGGGAG CGCGTGCTCA 550

ACGCGTCCGC CGAGGCTCAG CGCGCAGCCG CCCGGTTCCA CCAGCTGGAC 600

GTCAAGTTCC GCGAGCTGGC GCAGCTCGTC ACCCAGCAGA GCAGTCTCAT 650

CGCCCGCCTG GAGCGCCTGT GCCCGGGAGG CGCGGGCGGG CAGCAGCAGG 700

TCCTGCCGCC ACCCCCACTG GTGCCTGTGG TTCCGGTCCG TCTTGTGGGT 750

AGCACCAGTG ACACCAGTAG GATGCTGGAC CCAGCCCCAG AGCCCCAGAG 800

AGACCAGACC CAGAGACAGC AGGAGCCCAT GGCTTCTCCC ATGCCTGCAG 850

GTCACCCTGC GGTCCCCACC AAGCCTGTGG GCCCGTGGCA GGATTGTGCA 900

GAGGCCCGCC AGGCAGGCCA TGAACAGAGT GGAGTGTATG AACTGCGAGT 950

GGGCCGTCAC GTAGTGTCAG TATGGTGTGA GCAGCAACTG GAGGGTGGAG 1000

GCTGGACTGT GATCCAGCGG AGGCAAGATG GTTCAGTCAA CTTCTTCACT 1050

ACCTGGCAGC ACTATAAGGC GGGCTTTGGG CGGCCAGACG GAGAATACTG 1100

GCTGGGCCTT GAACCCGTGT ATCAGCTGAC CAGCCGTGGG GACCATGAGC 1150

TGCTGGTTCT CCTGGAGGAC TGGGGGGGCC GTGGAGCACG TGCCCACTAT 1200

FIG. 6A

GATGGCTTCT CCCTGGAACC CGAGAGCGAC CACTACCGCC TGCGGCTTGG 1250

CCAGTACCAT GGTGATGCTG GAGACTCTCT TTCCTGGCAC AATGACAAGC 1300

CCTTCAGCAC CGTGGATAGG GACCGAGACT CCTATTCTGG TAACTGTGCC 1350

CTGTACCAGC GGGGAGGCTG GTGGTACCAT GCCTGTGCCC ACTCCAACCT 1400

CAACGGTGTG TGGCACCACG GCGGCCACTA CCGAAGCCGC TACCAGGATG 1450

GTGTCTACTG GGCTGAGTTT CGTGGTGGGG CATATTCTCT CAGGAAGGCC 1500

GCCATGCTCA TTCGGCCCCT GAAGCTGTGA CTCTGTGTTC CTCTGTCCCC 1550

TAGGCCCTAG AGGACATTGG TCAGCAGGAG CCCAAGTTGT TCTGGCCACA 1600

CCTTCTTTGT GGCTCAGTGC CAATGTGTCC CACAGAACTT CCCACTGTGG 1650

ATCTGTGACC CTGGGCGCTG AAAATGGGAC CCAGGAATCC CCCCCGTCAA 1700

TATCTTGGCC TCAGATGGCT CCCCAAGGTC ATTCATATCT CGGTTTGAGC 1750

TCATATCTTA TAATAACACA AAGTAGCCAC 1780

FIG. 6B

```
Met Gly Lys Pro Trp Leu Arg Ala Leu Gln Leu Leu Leu Leu Leu
 1               5                  10                  15

Gly Ala Ser Trp Ala Arg Ala Gly Ala Pro Arg Cys Thr Tyr Thr
                20                  25                  30

Phe Val Leu Pro Pro Gln Lys Phe Thr Gly Ala Val Cys Trp Ser
                35                  40                  45

Gly Pro Ala Ser Thr Arg Ala Thr Pro Glu Ala Ala Asn Ala Ser
                50                  55                  60

Glu Leu Ala Ala Leu Arg Met Arg Val Gly Arg His Glu Glu Leu
                65                  70                  75

Leu Arg Glu Leu Gln Arg Leu Ala Ala Ala Asp Gly Ala Val Ala
                80                  85                  90

Gly Glu Val Arg Ala Leu Arg Lys Glu Ser Arg Gly Leu Ser Ala
                95                 100                 105

Arg Leu Gly Gln Leu Arg Ala Gln Leu Gln His Glu Ala Gly Pro
               110                 115                 120

Gly Ala Gly Pro Gly Ala Asp Leu Gly Ala Glu Pro Ala Ala Ala
               125                 130                 135

Leu Ala Leu Leu Gly Glu Arg Val Leu Asn Ala Ser Ala Glu Ala
               140                 145                 150

Gln Arg Ala Ala Ala Arg Phe His Gln Leu Asp Val Lys Phe Arg
               155                 160                 165

Glu Leu Ala Gln Leu Val Thr Gln Gln Ser Ser Leu Ile Ala Arg
               170                 175                 180

Leu Glu Arg Leu Cys Pro Gly Gly Ala Gly Gly Gln Gln Gln Val
               185                 190                 195

Leu Pro Pro Pro Pro Leu Val Pro Val Val Pro Val Arg Leu Val
               200                 205                 210

Gly Ser Thr Ser Asp Thr Ser Arg Met Leu Asp Pro Ala Pro Glu
               215                 220                 225

Pro Gln Arg Asp Gln Thr Gln Arg Gln Gln Glu Pro Met Ala Ser
               230                 235                 240

Pro Met Pro Ala Gly His Pro Ala Val Pro Thr Lys Pro Val Gly
               245                 250                 255
```

FIG. 7A

Pro Trp Gln Asp Cys Ala Glu Ala Arg Gln Ala Gly His Glu Gln
260 265 270

Ser Gly Val Tyr Glu Leu Arg Val Gly Arg His Val Val Ser Val
275 280 285

Trp Cys Glu Gln Gln Leu Glu Gly Gly Gly Trp Thr Val Ile Gln
290 295 300

Arg Arg Gln Asp Gly Ser Val Asn Phe Phe Thr Thr Trp Gln His
305 310 315

Tyr Lys Ala Gly Phe Gly Arg Pro Asp Gly Glu Tyr Trp Leu Gly
320 325 330

Leu Glu Pro Val Tyr Gln Leu Thr Ser Arg Gly Asp His Glu Leu
335 340 345

Leu Val Leu Leu Glu Asp Trp Gly Gly Arg Gly Ala Arg Ala His
350 355 360

Tyr Asp Gly Phe Ser Leu Glu Pro Glu Ser Asp His Tyr Arg Leu
365 370 375

Arg Leu Gly Gln Tyr His Gly Asp Ala Gly Asp Ser Leu Ser Trp
380 385 390

His Asn Asp Lys Pro Phe Ser Thr Val Asp Arg Asp Arg Asp Ser
395 400 405

Tyr Ser Gly Asn Cys Ala Leu Tyr Gln Arg Gly Gly Trp Trp Tyr
410 415 420

His Ala Cys Ala His Ser Asn Leu Asn Gly Val Trp His His Gly
425 430 435

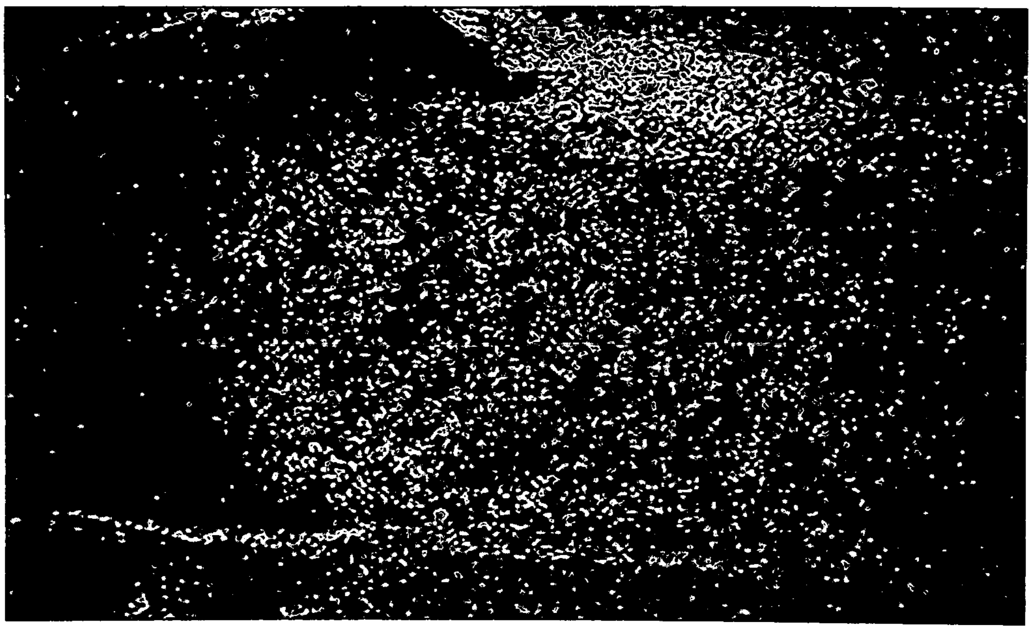
Gly His Tyr Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu
440 445 450

Phe Arg Gly Gly Ala Tyr Ser Leu Arg Lys Ala Ala Met Leu Ile
455 460 465

Arg Pro Leu Lys Leu
470

FIG. 7B

DNA 22779 DARK FIELD



THE WHITE SPOTS REPRESENT THE SILVER GRAINS.

FIG. 8A

DNA 22779 H&E

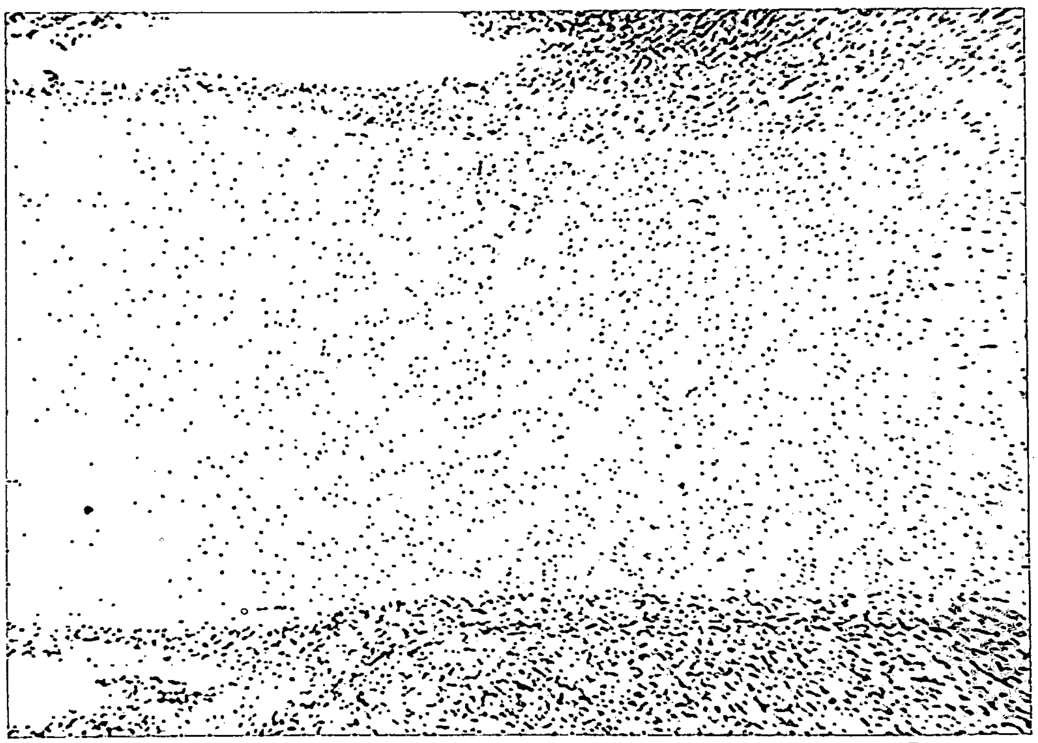


FIG. 8B

DNA 28497 H&E

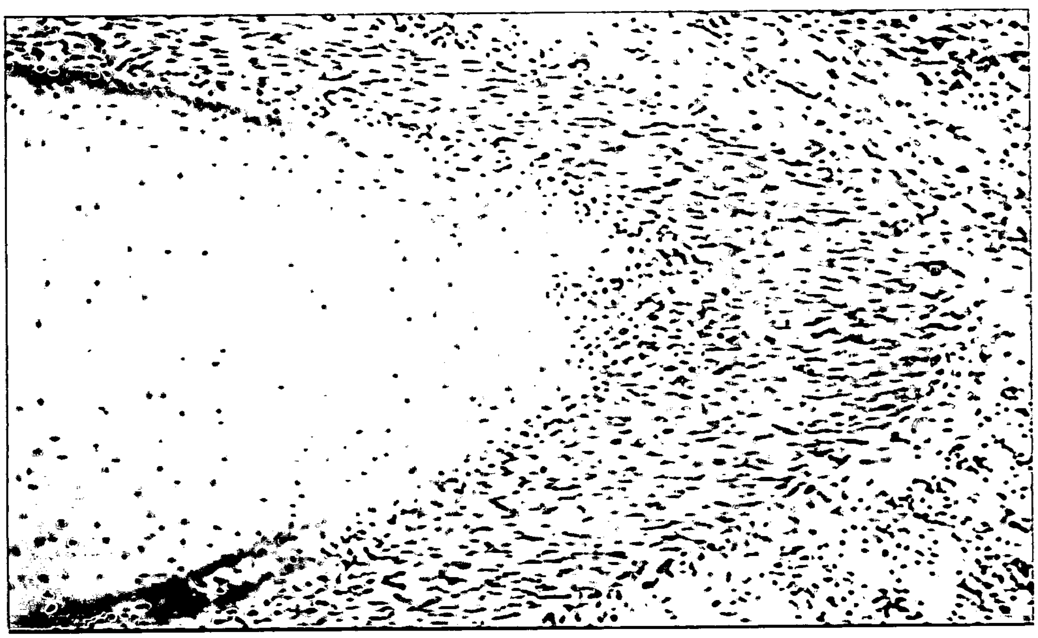
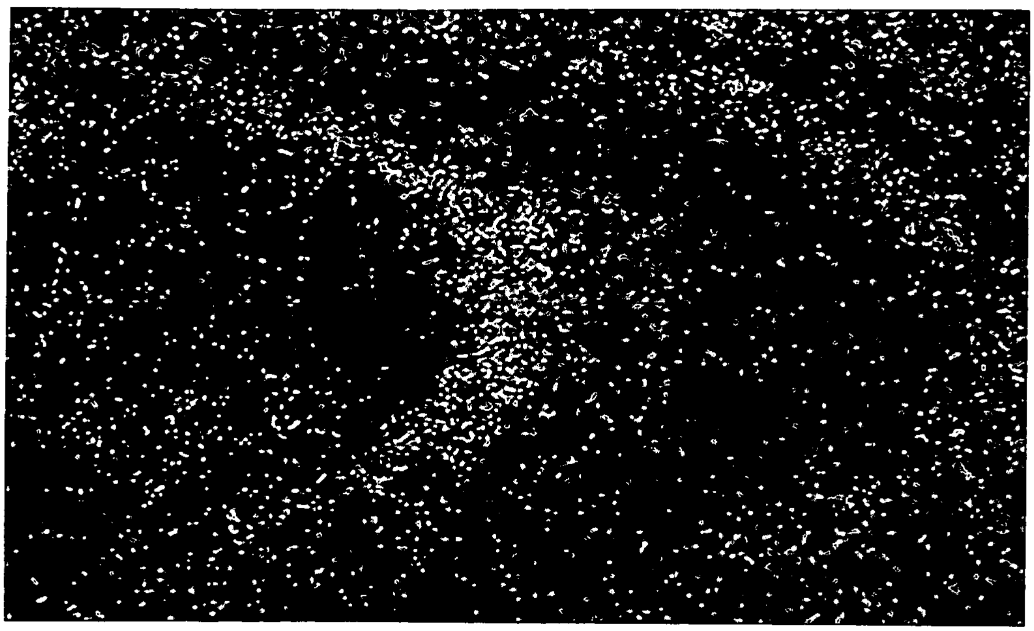


FIG. 9A

DNA 28497 DARK FIELD



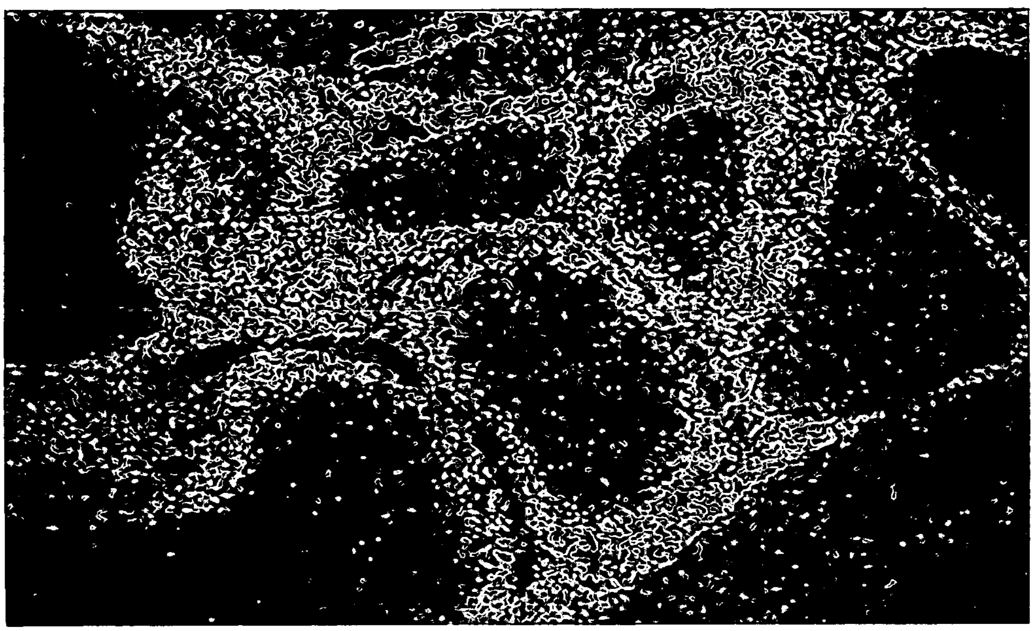
THE WHITE SPOTS REPRESENT THE SILVER GRAINS.

FIG. 9B

DNA 23339 H&E

FIG. 10A

DNA 23339 DARK FIELD



THE WHITE SPOTS REPRESENT THE SILVER GRAINS.

FIG. 10B

NL1 Northern

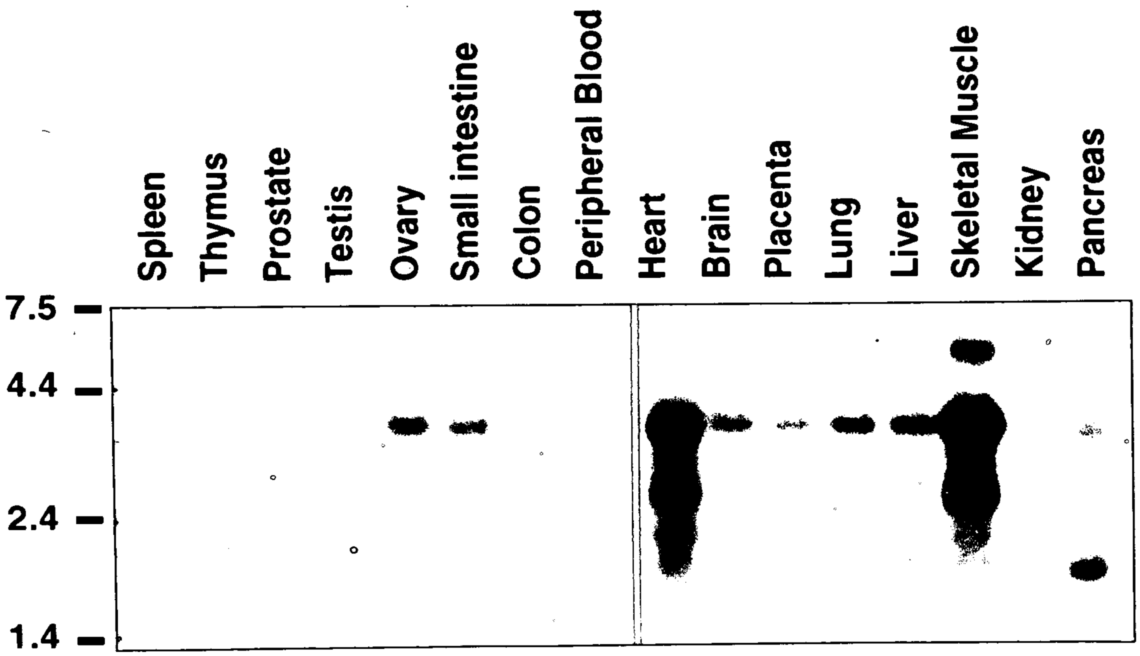


FIG. 11

NL5 Northern

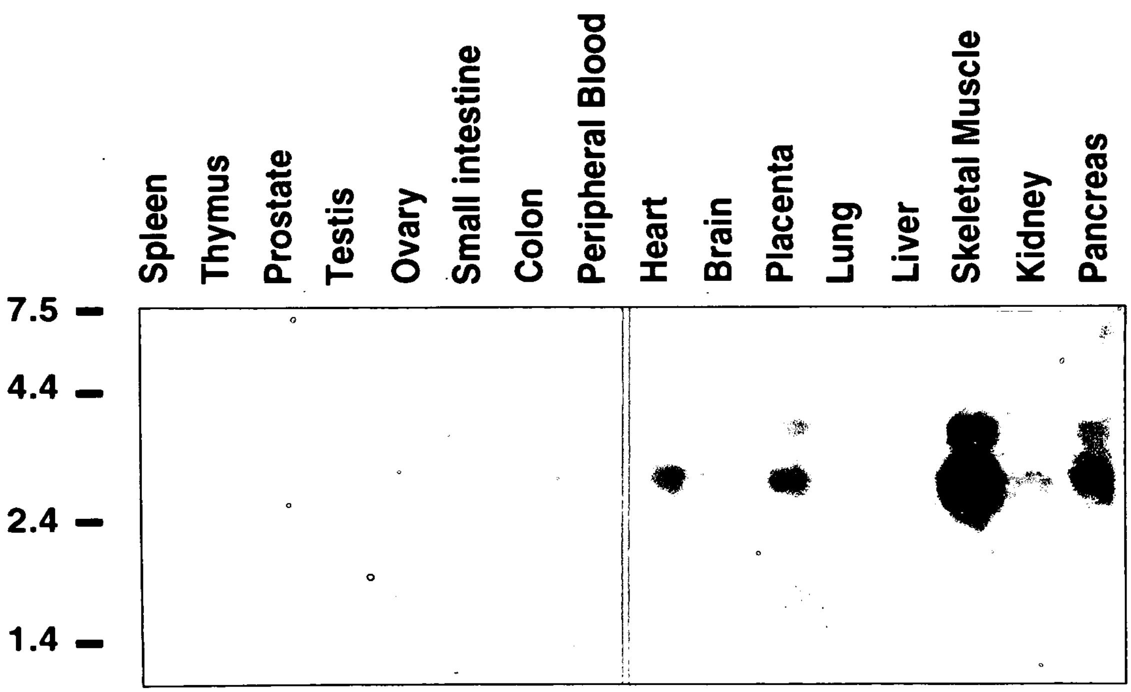


FIG. 12